SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANTS: BEAUDOIN, Adrien R. SÉVIGNY, Jean
- (ii) TITLE OF THE INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT TECHNOLOGY
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: GOUDREAU GAGE DUBUC & MARTINEAU WALKER
 - (B) STREET: 800 PLACE VICTORIA, SUITE 3400
 - (C) CITY: MONTREAL
 - (D) STATE: QUEBEC
 - (E) COUNTRY: CANADA
 - (F) ZIP: H4Z 1E9
 - (v) COMPUTER READABLE :
 - (A) MEDIUM TYPE: DISKETTE 1.44
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: WINDOWS 3.1
 - (D) SOFTWARE: WORDPERFECT 6.1
 - CURRENT APPLICATION DATA: (vi)
 - APPLICATION NUMBER:
 - (A) (B) FILING DATE: APRIL 10, 1996
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION: U.S.S.N 08/419,204
 - FILING DATE: APRIL 10, 1995 (B)
 - (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Jean H. DUBUC, Gaétan PRINCE, Alain M. LECLERC
- (C) REFERENCE/DOCKET NUMBER: DH/10857.146

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (514) 397-4335
- (B) TELEFAX: (514) 397-4382

(2) INFORMATION FOR SEQ ID NO: 1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
- Met Glu Asp Thr
 Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys

 Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile

 Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile

 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu

 Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr

 Asn Val Lys Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr

 Fell Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly

 Asn Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly

 Fell Ser Lys Phe Val Glu Arg Ala Arg Glu Val Ile Gly Ile Tyr Leu Gly

 His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg

 Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp

 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile 180
Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp 195 196
Thr Ile Asn Tyr Leu Leu G1/ -1 190 185
185 Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly 210
200 200 Thr Gln Val Thr Phe Val Pro
200 Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro 225 220 226
215 215 Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg 240 230 230 230
230 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys 255 265 265 265 265 275 275 275 275 275 275 275 275 275 27
245 Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile 270 260 265 270 260 270 270 270 270
260 Clin Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro 285 280 287
275 Cly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro 300 295
290 Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu 315
Cys Thr Lys Arg Phe Glu Met III 1860 315
305 305 Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu 330 330 330
320 325 Tyr Ser Gln Cys Ala Phe
320 320 Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe 345
Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe 360 355 360
Ash Gly 116 116 350 355 350 Leu Ash Leu Thr Ser Glu
350 Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu 375 370
365 Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys 390
Lys Val Ser Gin 322 27 385 380 385 Tur Ala Gly Val Lys
380 380 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys 405
395 Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu 420 415
Glu Lys Tyr Leu Sei Glu -1- 415 410 410 415
410 410 Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu 435 436 437
425 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp 450 440 445 450 460
440 440 Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu 465
455 Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu 480
Gln Pro Leu Ser Thr Pro Leu Ser Mas 475

 Met
 Val
 Leu
 Phe
 Ser
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 Leu
 Phe
 Thr
 Val
 Ala
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 Gly

 Leu
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(2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

(X1) SEQUENCE - ACACCAGGAA AGAGGAGGAA	50
ACCACACAA GCAGCGGCTG GGGGGGGAA AGACGAGGAA AGAGGAGGAA ACCACACAA GCAGCGGCTG GGGGGGGGAA AGACGAGAGACA AGGAGTCTAA CGTGAAGACA	100
ACCACACCAA GCAGCGGCTG GGGGGGGGAA AGACCATCATAA CGTGAAGACA AACAAAAGCT GCTACTTATG GAAGATACAA AGGAGTCTAA CGTGAAGACA AACAAAAGCT GCTACTTATG AGGCATCCTT GGCTTCTCCT CTATCATAGC	150
TTTTGCTCCA AGAATATCCT AGCCATCACA CCAGAACAAA GCATTGCCAG	200
TGTGATAGCT TTGCTTGCTG TGGGGTTGAC CCCCTTCTTC TCACACAAGT	250
AAAACGTTAA GTATGGGATT GTGCTGGATG CGGGTTGT	300
TTATACATCT ATAAGTGGCC AGCAGAAAAA TTG	350
GCATCAAGTA GAAGAATGCA GGGTTAAAGG TCACTGATTG CATGGAAAGA	400
TTCAGAAAGT AAATGAAATA GGCATTACC CAAGAGACAC CCGTTTACCT	450
GCTAGGGAAG TGATTCCAAG GICCCAGCAC CATGGAAAGT GAAGAGTTGG	500
GGGAGCCACG GCAGGCATGC GGTTGCTCAGCAA CTACCCCTTT	550
CAGACAGGGT TCTGGATGTG GTGGAGAGGA GTGCCTATGG	600
GACTTCCAGG GTGCCAGGAT CATTACTGGC GTCAG AAAACAAGGT	650
CTGGATTACT ATCAACTATC TGCTGGGATTA ATCAGGATAC CTTTGGAGCT	700
GGTTCAGCAT AGTCCCATAT GAAACCAATA ACTTTTGTAC CCCAAAACCA	750
TTGGACCTTG GGGGAGCCTC TACACAAGTG ATTTCGCCTC TATGGCAAGG	800
GACTATCGAG TCCCCAGATA AIGCICATEGGAA GGATCAGGCA	850
	900
CTCTGGCAGA AACTGGCCAA GGACATTCAG GIIGCIATO CAGGGACCCA TGCTTTCATC CTGGATATAA GAAGGTAGTG AACGTAAGTG CAGGGACCCA TGCTTTCATC ACCAAGAGT TTGAGATGAC TCTTCCATTC	950
CAGGGACCCA TGCTTTCATC CIGGALATE TTGAGATGAC TCTTCCATTC	1000
ACCTTTACAA GACCCCCTGC ACCAAGAGAT TIGAGATOTA ACCTTTACAA GACCCCCTGC ACCAAGAGAT TIGAGATAT GCCATCAAAG CAGCAGTTTG AAATCCAGGG TATTGGAAAC TATCAACAAT GCCATCAAAG CAGCAGTTTACTG CCCTTACTCC CAGTGTGCCT	1050
CAGCAGTTTG AAATCCAGGG TATTGGAAAC TATCATCC CAGTGTGCCT CATCCTGGAG CTCTTCAACA CCAGTTACTG CCCTTACTCC CAGTGTGCCT CATCCTGGAG CTCTTCAACA CCAGTTCCAGG GGGATTTTGG GGCATTTTCA	1100
CATCCTGGAG CTCTTCAACA CCAGTTACTG CCCTTTTTGG GGCATTTTCA TCAATGGGAT TTTCTTGCCA CCACTCCAGG GGGATTTTGG GGCATTTTCA	1150
	1200
	1250
TCAGGAAAAG GTGACTGAGA TGATGAAAAA GTTGTGTGAAAAA GTTGTGTGAAAAA AACATCTTAC GCTGGAGTAA AGGAGAAGTA CCTGAGTGAAAAA GTTGTGTGAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAA GTTGTGTGAAAAAAA GTTGTGTGAAAAAAAA	1300
AGGAGATAAA AACATUTTAC GCTCOAC	

THE COMMON OF THE PROPERTY OF	ATCA 1350
TACTGCTTTT CTGGTACCTA CATTCTCTCC CTCCTTCTGC AAGGCTA	TAGG 1400
TACTGCTTTT CTGGTACCTA CATTCTCTCC CTCGTATGC AAGATCC TTTCACAGCT GATTCCTGGG AGCACATCCA TTCATTGGC AAGATCC	CATC 1450
TTTCACAGCT GATTCCTGGG AGCACATCCA TTTCACAGCT GACCAAGGCGACGC CGGCTGGACT TTGGGCTACA TGCTGAACCT GACCAAG	TATG 1500
GCAGCGACGC CGGCTGGACT TTGGGGTACA CTCTCCCACT CCACCT	ATGT 1500
GCAGCGACGC CGGCTGGACT TTGGGCTACA TGCTGACACT CCACCT. ATCCCAGCTG AGCAACCATT GTCCACACCT TTTCACAGTG GCCATC	ATAG 1550
ATCCCAGCTG AGCAACCATT GTCCACACCT CTCTGACAGTG GCCATC CTTCCTCATG GTTCTATTCT CCCTGGTCCT TTTCACAGTG GCCATC	ATAG 1600
CTTCCTCATG GTTCTATTCT CCCTGGTCCT TTGTGTAAAGA TATGGT GCTTGCTTAT CTTTCACAAG CCTTCATATT TCTGGAAAAAA TCGTCC	AGGG 1650
GCTTGCTTAT CTTTCACAAG CCTTCATATT TCTGGTTCCCCCCCCCC	1700 1700
CAAAAGCAGC TGAAATATGC TGGCTGGAGT GAGGTTTCCC TGTCTG AGCATTTCC TCCATCGCAG TGTTCAAGGC CATCCTTCCC TGTCTG AGCATTTCCT GGCTTTTACT GAAGCC	1750
AGCATTTTCC TCCATCGCAG TOTTGCTT GGCTTTTACT GAAGCC	TTTC 1/30
AGCATTTCC TCCATCGCAG TGTTCAAGGC CATCGTTACT GAAGCC GGCCAGTCTT GACGAGTGTG AAGCTTCCTT AGGACTTCGG CAGATA	CTGT 1800
GGCCAGTCTT GACGAGTGTG AAGCTTCCTT GGCTTTTTTTTTT	1818
CTCTTTCATG AGTTTTTC	

- (2) INFORMATION FOR SEQ ID NO: 3
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 AMINO ACIDS .
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
5 10

- (2) INFORMATION FOR SEQ ID NO: 4
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

Leu Leu Arg Met Glu

5

(2) INFORMATION FOR SEQ ID NO: 5

(i) SE	QUENCE CHARACTERISTICS:
. (A) LENGTH: 13 AMINO ACIDS
10	B) TYPE: AMINO ACID C) STRANDEDNESS: SINGLE C) TOPOLOGY: LINEAR
	EQUENCE DESCRIPTION: SEQ ID NO: 5
Ala Asp Lys	Ile Leu Ala Asn Xaa Val Ala Ser Ser Ile 5
(2) INFORM	ATION FOR SEQ ID NO: 6
(i) S	SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 10 AMINO ACIDS (B) TYPE: AMINO ACID (C) STRANDEDNESS: SINGLE (D) TOPOLOGY: LINEAR
\ /	SEQUENCE DESCRIPTION: SEQ ID NO: 6
Tyr Pro Ph	ne Asp Phe Gln Gly Ala Arg Ile 5
(2) INFO	RMATION FOR SEQ ID NO: 7
(i)	SEQUENCE CHARACTERISTICS:
	 (A) LENGTH: 20 AMINO ACIDS (B) TYPE: AMINO ACID (C) STRANDEDNESS: SINGLE (D) TOPOLOGY: LINEAR
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7
Lys Ser I	Asp Thr Gln Glu Thr Tyr Gly Ala Leu Asp Leu Gly Gly 15
Ala Ser	Thr Gln Val

- (2) INFORMATION FOR SEQ ID NO: 8
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

Lys Ser Asp Thr Gln Glu Thr Tyr Gly Ala Leu Asp Leu Gly Gly
5 10 15